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FASTA searches a protein or DNA sequence data bank
 version 3.4t10 Dec 12, 2001

Please cite:

W. R. Pearson & D. J. Lipman PNAS (1988) 85:2444-2448

/tmp/WWW/get_linkdb_fasta.25159/b3823: 122 aa
 >eco:b3823 yigJ; hypothetical 22.5 kD protein in recQ-mlD Intergenic region (A)
 vs /bio/db/fasta/genes/genes library
 searching /bio/db/fasta/genes/genes library

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inset = represents 15 library sequences

BEST AVAILABLE COPY

Search Result: eco:b3823 -> GENES

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110 101 48:* :==*==*
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114 44 29:* :==*
116 38 22:* :==*
118 32 17:* :==*
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257957986 residues in 729837 sequences

statistics extrapolated from 60000 to 729458 sequences

Expectation_n fit: rho(ln(x)) = 3.2816+/-0.000168; mu = 15.2431+/-0.017

mean_var=57.4751+/-11.689, 0's: 0 Z-trim: 3 B-trim: 3787 in 1/58

Lambda= 0.1692

Kolmogorov-Smirnov statistic: 0.0430 (N=29) at 50

FASTA (3.44 Dec 2001) function [optimized, BL50 matrix (15:-5)] ktup: 2

join: 36, opt: 24, open/ext: -10/-2, width: 16

Scan time: 89.390

The best scores are:

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Search Result: eco:b3823 -> GENES

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<input type="checkbox"/> ban:BA2355	homoserine/threonine efflux protein, putative	(210)	150	44 0. 001
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Search Result: eco:b3823 -> GENES

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<input type="checkbox"/> vpa:VPA1232	conserved hypothetical protein	(204)	111	35	0.72
<input type="checkbox"/> atc:AGR_L_2738	conserved hypothetical protein	(278)	112	35	0.73
<input type="checkbox"/> pae:PA5341	hypothetical protein	(206)	111	35	0.73
<input type="checkbox"/> cyl:CYL042	probable amino acid efflux protein	(209)	111	35	0.73
<input type="checkbox"/> sme:SMc03827	putative amino acid efflux transmembrane prot	(213)	111	35	0.74
<input type="checkbox"/> oja:OB0964	hypothetical conserved protein	(171)	109	34	0.92

>>[eco:25344](#) yigJ; orf; Unknown function (122 aa)
 initn: 792 initl: 792 opt: 792 Z-score: 1053.8 bits: 200.4 E() : 5e-51
 Smith-Waterman score: 792; 100.000% identity (100.000% ungapped) in 122 aa overlap (1-122:1-122)

10	20	30	40	50	60	70
eco:b3	MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIYFGSVFSLFVGDNVGT TARW GIFA	:	:	:	:	:
eco:25	MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIYFGSVFSLFVGDNVGT TARW GIFA	:	:	:	:	:
10	20	30	40	50	60	70

80	90	100	110	120
eco:b3	LII VETLAWFTTVASLFA LPQMRRGYQRLAKWIDGFAGALFAGFGIHLIISR	:	:	:
eco:25	LII VETLAWFTTVASLFA LPQMRRGYQRLAKWIDGFAGALFAGFGIHLIISR	:	:	:
80	90	100	110	120

>>[eco:b3823](#) yigJ; hypothetical 22.6 kD protein in recQ-pldB inter (122 aa)
 initn: 792 initl: 792 opt: 792 Z-score: 1053.8 bits: 200.4 E() : 5e-51
 Smith-Waterman score: 792; 100.000% identity (100.000% ungapped) in 122 aa overlap (1-122:1-122)

10	20	30	40	50	60	70
eco:b3	MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIYFGSVFSLFVGDNVGT TARW GIFA	:	:	:	:	:
eco:b3	MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIYFGSVFSLFVGDNVGT TARW GIFA	:	:	:	:	:
10	20	30	40	50	60	70

80	90	100	110	120
eco:b3	LII VETLAWFTTVASLFA LPQMRRGYQRLAKWIDGFAGALFAGFGIHLIISR	:	:	:
eco:b3	LII VETLAWFTTVASLFA LPQMRRGYQRLAKWIDGFAGALFAGFGIHLIISR	:	:	:
80	90	100	110	120

>>[ecj:JW3797](#) yigJ; Amino acid exporter (threonine) (155 aa)
 initn: 799 initl: 799 opt: 792 Z-score: 1052.7 bits: 200.6 E() : 5.7e-51
 Smith-Waterman score: 792; 100.000% identity (100.000% ungapped) in 122 aa overlap (1-122:34-155)

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ZU04 09/06 H 19:32 PAA 分析行式表示用

XW3001

WU20/000
21/ 04

Search Result: eco:b3823 -> GENES

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	10	20	30
eco:b3	MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLT		

	10	20	30	40	50	60	70
ecj:JW	LGHDCAAWPAFDYRKNGLAAYADYGGRWLYLCMAGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLT						

	40	50	60	70	80	90	100
eco:b3	NLANPKAIIYFGSVFSLFVGDNVGTARWGIFALIIIVETLAWFTVVASLFA[P]QMRRGYQRLAKWIDGFA						

	80	90	100	110	120	130	140
ecj:JW	NLANPKAIIYFGSVFSLFVGDNVGTARWGIFALIIIVETLAWFTVVASLFA[P]QMRRGYQRLAKWIDGFA						

	110	120
eco:b3	GALFAGFGIHLIISR	

	150	
ecj:JW	GALFAGFGIHLIISR	

>>ecs:ECs4763 threonine efflux protein (KO:K03329) (206 aa)
 initn: 799 initl: 799 opt: 792 Z-score: 1051.5 bits: 200.8 E 0 : 6.7e-51
 Smith-Waterman score: 792; 100.000% identity (100.000% ungapped) in 122 aa overlap (1-122:85-206)

	10	20	30
eco:b3	MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL		

	50	60	70	80	90	100	110
ecs:EC	MVWAGIALLGLHLIEKHAWLHTLIMVGGGLYLCLAGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL						

	40	50	60	70	80	90	100
eco:b3	LTNLANPKAIIYFGSVFSLFVGDNVGTARWGIFALIIIVETLAWFTVVASLFA[P]QMRRGYQRLAKWIDG						

	120	130	140	150	160	170	180
ecs:EC	LTNLANPKAIIYFGSVFSLFVGDNVGTARWGIFALIIIVETLAWFTVVASLFA[P]QMRRGYQRLAKWIDG						

	110	120
eco:b3	FAGALFAGFGIHLIISR	

	190	200
ecs:EC	FAGALFAGFGIHLIISR	

>>sfx:S3854 yigJ: hypothetical protein (122 aa)
 initn: 786 initl: 786 opt: 786 Z-score: 1045.9 bits: 199.0 E 0 : 1.4e-50
 Smith-Waterman score: 786; 99.180% identity (99.180% ungapped) in 122 aa overlap (1-122:1-122)

	10	20	30	40	50	60	70
eco:b3	MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLTNLANPKAIIYFGSVFSLFVGDNVGTARWGIFA						

	10	20	30	40	50	60	70
sfx:S3	MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLTNLANPKAIIYFGSVFSLFVGDNVGTTERWGIFA						

	80	90	100	110	120
eco:b3	LIIIVETLAWFTVVASLFA[P]QMRRGYQRLAKWIDGFAGALFAGFGIHLIISR				

	80	90	100	110	120
sfx:S3	LIIIVETLAWFTVVASLFA[P]QMRRGYQRLAKWIDGFAGALFAGFGIHLIISR				

>>sfx:SF3901 rhtC; threonine efflux protein (206 aa)
 initn: 793 initl: 793 opt: 786 Z-score: 1043.6 bits: 199.3 E 0 : 1.9e-50
 Smith-Waterman score: 786; 99.180% identity (99.180% ungapped) in 122 aa overlap (1-122:85-206)

	10	20	30
eco:b3	MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL		

	50	60	70	80	90	100	110
sfx:SF	MVWAGIALLGLHLIEKHAWLHTLIMVGGGLYLCLAGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL						

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ZUU4 09/00 H 19:33 MAI 分割付与申請用
V4- 0-20; 0:4040M:0000000000000000

WU42443013 R 42/ 54

Search Result: eco:b3823 → GENES

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40	60	60	70	80	90	100	
eco:b3 LTNLANPKAI YFGSVFSLFVGDNVGTARWG FAL VETLAWFTVVASLFA PQMRRGYQRLAKW DG	120	130	140	150	160	170	180

110	120						
eco:b3 FAGALFAGFGIHLIISR	190	200					
sfl:SF LTNLANPKAI YFGSVFSLFVGDNVCTTERWG FAL VETLAWFTVVASLFA PQMRRGYQRLAKW DG	120	130	140	150	160	170	180

>>ecc:c4745 threonine efflux protein [KO:K03328] (206 aa)
 initn: 788 initl: 788 opt: 781 Z-score: 1097.0 bits: 198.1 E 0 : 4.3e-50
 Smith-Waterman score: 781: 98.361% identity (98.361% ungapped) in 122 aa overlap (1-122:85-206)

10	20	30					
eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL	50	60	70	80	90	100	110
scc:c4 MVWAGIALLGLHLIIEKMAWLHTI MVGGLYLCHMGYQMLRGALKKEVVSAPAPQVELAKSGRSFLKGL	120	130	140	150	160	170	180

40	50	60	70	80	90	100	
eco:b3 LTNLANPKAI YFGSVFSLFVGDNVGTARWG FAL VETLAWFTVVASLFA PQMRRGYQRLAKW DG	120	130	140	150	160	170	180
scc:c4 LTNLANPKAI YFGSVFSLFVGDNVCTTERWG FAL VETLAWFTVVASLFA PQMRRGYQRLAKW DG	120	130	140	150	160	170	180

110	120						
eco:b3 FAGALFAGFGIHLIISR	190	200					
scc:c4 FAGALFAGFGIHLIISR	120	130	140	150	160	170	180

>>stm:STM3959 rhtC; RhtB family, threonine efflux protein (206 aa)
 initn: 724 initl: 724 opt: 717 Z-score: 952.6 bits: 182.5 E 0 : 2.2e-45
 Smith-Waterman score: 717: 87.705% identity (87.705% ungapped) in 122 aa overlap (1-122:85-206)

10	20	30					
eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL	50	60	70	80	90	100	110
stm:ST MVWAGVALLGLHLIIEKMAWLHTI MVGGLYLCHMGYQMLRGALKKDAASSPHIELAQSGRSFLKGL	120	130	140	150	160	170	180

40	50	60	70	80	90	100	
eco:b3 LTNLANPKAI YFGSVFSLFVGDNVGTARWG FAL VETLAWFTVVASLFA PQMRRGYQRLAKW DG	120	130	140	150	160	170	180
stm:ST LTNLSNPKAIIYFGSVFSLFVGDNVGAARWG FALITLETLAWFTVVASLFA PQMRRGYQRLAKW DG	120	130	140	150	160	170	180

110	120						
eco:b3 FAGALFAGFGIHLIISR	190	200					
stm:ST FAGALFAGFGIHLIISR	120	130	140	150	160	170	180

>>sty:STY3600 rhtC; threonine efflux protein [KO:K03329] (206 aa)
 initn: 724 initl: 724 opt: 717 Z-score: 952.6 bits: 182.5 E 0 : 2.2e-45
 Smith-Waterman score: 717: 87.705% identity (87.705% ungapped) in 122 aa overlap (1-122:85-206)

10	20	30					
eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL	50	60	70	80	90	100	110
sty:ST MVWAGVALLGLHLIIEKMAWLHTI MVGGLYLCHMGYQMLRGALKKDAASSPHIELAQSGRSFLKGL	120	130	140	150	160	170	180

http://www.genome.jp/tmp/get_linkdb_fasta.25159/result_genes.html

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ZUUU9 U9/UU M 19:00 PM 7月19日 月曜日
U4- 8-25; D:40PM:時間(日)月曜日セレク四 UU/UU
R 23/ 34

Search Result: eco:b3823 -> GENES

SRR5507

JUN42449019

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50 60 70 80 90 100 110

40 50 60 70 80 90 100
 eco:b3 LTNILANPKAIYFGSVFSLFVGDNVGTARWGIFALIIVETLAWFTVVASLFA
 sty:ST LTNLSNPKAIIYFGSVFSLFVGDNVGAARWGIFALITLETLAWFTVVASLFA
 120 130 140 150 160 170 180

110 120
 eco:b3 FAGALFAGFGIHLIISR
 sty:ST FAGALFAGFGIHLIISR
 190 200

>>st:t3338 rhtC: threonine efflux protein [KO:K03329] (206 aa)
 initn: 724 init1: 724 opt: 717 Z-score: 852.6 bits: 182.5 E 0 : 2.2e-45
 Smith-Waterman score: 717; 87.705% identity (87.705% ungapped) in 122 aa overlap (1-122:85-206)

10 20 30
 eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL
 stt:t3 VVWAGVALLGLHLIIEKMAWLHTIMVGGGLYLCHMGYQMLRGALKKKDAASSPHIELAQSGRSFLKGL
 50 60 70 80 90 100 110

40 50 60 70 80 90 100
 eco:b3 LTNILANPKAIYFGSVFSLFVGDNVGTARWGIFALIIVETLAWFTVVASLFA
 stt:t3 LTNLSNPKAIIYFGSVFSLFVGDNVGAARWGIFALITLETLAWFTVVASLFA
 120 130 140 150 160 170 180

110 120
 eco:b3 FAGALFAGFGIHLIISR
 stt:t3 FACALFACFGIHLIISR
 190 200

>>eca:EC4171 rhtC: threonine efflux protein (207 aa)
 initn: 577 init1: 533 opt: 561 Z-score: 746.8 bits: 144.4 E 0 : 6.3e-34
 Smith-Waterman score: 561; 66.667% identity (67.213% ungapped) in 123 aa overlap (1-122:85-207)

10 20 30
 eco:b3 MGYQMLRGALKKEAV-SAPAPQVELAKSGRSFLKG
 eca:EC VVAAIAALLGLHLLLQKQWNLHTATVGGGLYLCHMGWQLRSARSQLETTQETAVLPQRGKTFMRG
 50 60 70 80 90 100 110

40 50 60 70 80 90 100
 eco:b3 LLTNILANPKAIYFGSVFSLFVGDNVGTARWGIFALIIVETLAWFTVVASLFA
 eca:EC LLTNILANPKAIYFGSVFSLFVGDSVGSARWGLFALISIETLLWFSLVAIVFALPTMRRGYQRLAKWVD
 120 130 140 150 160 170 180

110 120
 eco:b3 GFAGALFAGFGIHLIISR
 eca:EC GVAGVLFTGFGLHLIFSR
 190 200

>>ypm:YP3216 rhtC: threonine efflux protein (206 aa)
 initn: 567 init1: 567 opt: 560 Z-score: 745.5 bits: 144.1 E 0 : 7.5e-34
 Smith-Waterman score: 560; 67.213% identity (67.213% ungapped) in 122 aa overlap (1-122:85-206)

10 20 30
 eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGL
 50 60 70 80 90 100 110

http://www.genome.jp/tmp/get_linkdb_fasta.25159/result_genes.html

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Search Result: eco:b3823 → GENES

pmu:PM LFHALASILGLA|LFNTVPVLQQLVMTLGGGYLAYLGYLMLKS—QQNVVFEPYSEQEQNKQTSIKKEIT
50 60 70 80 90 100 110

eco:b3 KGLLTNLANPKAI|YFGSVFSLFVGDNVGTARWGI|FAL|VETLAWFTVVASLFLAPQMRGGYQRLAKV
40 50 60 70 80 90 100

pmu:PM KGLLVNLNAKAVIYFASVMSLVLVNLQTQWQSALLIVLETFLFYAI|SIVFSRQQAKQFYSQYSRY
120 130 140 150 160 170 180

eco:b3 1DGFAAGALFAGFGIHLIISR
110 120

pmu:PM 1DHLSGVIFLLFGVYLMYSGIGEMTPLISK
190 200 210

>>pha:BH2932 unknown conserved protein (210 aa)
initn: 221 initl: 221 opt: 229 Z-score: 308.8 bits: 63.4 E 0 : 1.6e-09
Smith-Waterman score: 229; 32.540% identity (34.167% ungapped) in 126 aa overlap (1-120:82-207)

eco:b3 10 20
MGYQMLRGAL-KKEAV—SAPAPQVELAKSG-R

bha:BH 1VHITYTVLGFATIETYPALFFT|QLLGAAYLIWLGPHAIRSSPPKKEEAEIEETQPIQSTKDSKSSIQ
50 60 70 80 90 100 110

eco:b3 30 40 50 60 70 80 90
SFLKGLLTNLANPKAI|YFGSVFSLFVGDNVGTARWGI|FAL|VETLAWFTVVASLFLAPQMRGGYQRL

bha:BH GFKEGFITNLLNPKAALFFLSIFSQF|TPQTADWVRHHMYGLEVVAVGLWFSFLAFISYKHFRRFYQTH
120 130 140 150 160 170 180

eco:b3 100 110 120
AKWIDGFAAGALFAGFGIHLIISR

bha:BH SYWFDRFLGAALLFFAIRIIIGAF
190 200 210

>>pst:PSPT02958 rhtC: threonine efflux protein (214 aa)
initn: 228 initl: 229 opt: 227 Z-score: 306.1 bits: 62.9 E 0 : 2.2e-09
Smith-Waterman score: 227; 33.628% identity (34.862% ungapped) in 113 aa overlap (12-120:93-205)

eco:b3 10 20 30 40
MGYQMLRGALKKEAVSAPAPQ—VELAKSGRSFLKGLLTNLANP

pst:PS AATGLGLVFEQLPWLPALQQLGGAYLTWLTQTKSLRSAGSQPKPRDVGALGIGSLSRAYRGLLTNLTP
60 70 80 90 100 110 120

eco:b3 50 60 70 80 90 100 110
KAIIYFGSVFSLFVGDNVGTARWGI|FAL|VETLAWFTVVASLFLAPQMRGGYQRLAKWIDGFAAGALFA

pst:PS KALAFYTSVFTTTPGMPMIVRTAGVSI|AVLAISWFVLLATLFS|PAVQARYQRMMKAIDIVTGLFWI
130 140 150 160 170 180 190

eco:b3 120
GFGIHLIISR

pst:PS AFGLRLLIGLLPTGVFH
200 210

>>bms:BR1920 transporter, LysE family (212 aa)
initn: 209 initl: 209 opt: 221 Z-score: 298.2 bits: 61.4 E 0 : 6.1e-09
Smith-Waterman score: 221; 32.231% identity (33.621% ungapped) in 121 aa overlap (1-118:88-206)

10 20 30

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Search Result: eco:b3823 -> GENES

eco:b3

MGYQMLR-GALKKEAVSAPAPQVELAKSG-RSFL

bms:BR MMHVTYTVLGLGLIISRSIYLFIIVKWCGVAYLVYIGFKALRAGTTKIEA-GPDKEPRRKQGFKAFCG
60 70 80 90 100 110 12040 50 60 70 80 90 100
eco:b3 KGLLTNLANPKAIYFGSVFSLFVGDNVGTARWGIHALIIVETLAWFTVVASLFAFPQMRGGYQRLAKW
130 140 150 160 170 180 190bms:BR LGFAANALNPKAFFLSIFSTVVHVHTPTEVKLGYGVVATLISWFVGVSFFMTPKRAAFSRASKW
130 140 150 160 170 180 190110 120
eco:b3 IDGFAGALFAGFGIHLIISRbms:BR IDRTSGVVVFIALGLKLATEKAM
200 210>>bme:BME10143 threonine efflux protein (212 aa)
initn: 209 initl: 209 opt: 221 Z-score: 298.2 bits: 61.4 E0: 6.1e-09
Smith-Waterman score: 221: 32.231% identity (33.621% ungapped) in 121 aa overlap (1-118:88-206)eco:b3 10 20 30
MGYQMLR-GALKKEAVSAPAPQVELAKSG-RSFLbme:BME MMHVTYTVLGLGLIISRSIYLFIIVKWCGVANLYVYIGFKALRAGTTKIEA-GPDKEPRRKQGFKAFCG
60 70 80 90 100 110 12040 50 60 70 80 90 100
eco:b3 KGLLTNLANPKAIYFGSVFSLFVGDNVGTARWGIHALIIVETLAWFTVVASLFAFPQMRGGYQRLAKW
130 140 150 160 170 180 190bme:BME LGFAANALNPKAFFLSIFSTVVHVHTPTEVKLGYGVVATLISWFVGVSFFMTPKRAAFSRASKW
130 140 150 160 170 180 190110 120
eco:b3 IDGFAGALFAGFGIHLIISRbme:BME IDRTSGVVVFIALGLKLATEKAM
200 210>>hin:HI1307 hypothetical protein HI1307 [KO:K03329] (210 aa)
initn: 203 initl: 203 opt: 220 Z-score: 296.9 bits: 61.2 E0: 7.2e-09
Smith-Waterman score: 220: 36.000% identity (39.474% ungapped) in 125 aa overlap (1-119:82-201)eco:b3 10 20 30
MGYQMLR-GALKKEAVSAPAPQVELAKSG-RSFLhin:HI AFVGMSLGLAFLFTIPALHGVIMLLGGSYLAYLGFIMARS-KKYAKFESHSDTEFNQQTTIKKEIL
50 60 70 80 90 100 11040 50 60 70 80 90 100
eco:b3 KGLLTNLANPKAIYFGSVFSLFVGDNVGTARWGIHALIIVETLAWFTVVASLFAFPQMRGGYQRLhin:HI KGLLVNLSNAKVVVFSSVMSLVL-VNITEHQIIIAFAVIVVETFCYFYVVISLIFSRNIAKRLYSQY
120 130 140 150 160 170 180100 110 120
eco:b3 AKWIDGFAGALFAGFGIHLIISRhin:HI SRYIDNMAGIVFLFFGCVLVYNGINEIIH
190 200 210>>psr:PSPT01147 transporter, LysE family (210 aa)
initn: 213 initl: 213 opt: 216 Z-score: 291.7 bits: 60.2 E0: 1.4e-08
Smith-Waterman score: 216: 28.689% identity (28.926% ungapped) in 122 aa overlap (1-121:86-207)

Search Result: eco:b3823 → GENES

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eco:b3 10 20 30
MGYQMLRGALKKEAVSAPAPQVELAKSGR-SFLKG

psl:PS FVHVGYSLLGIGIIVSQSIVLFRNALKWAAAAYLLYIGIKALRAKPAATDDTAIKAVAGERSARGAYISG
60 70 80 90 100 110 120

eco:b3 40 50 60 70 80 90 100
LLTNLANPKAIYFGSVFSLFVGDNVGTARWGIHALIIVETLAWFTVVASLFA
psl:PS FVTNGLNPKATLFFLSLFTVWINPHTPLLWQGGYGVYLAVATAAWFC
130 140 150 160 170 180 190

eco:b3 110 120
GFAGALFAGFGIHLISR

psl:PS RAMGGVLVALGIKLALTEVR
200 210

>>cdi:DIP1767 putative LysE type translocator (212 aa)
initn: 211 initl: 217 opt: 216 Z-score: 291.6 bits: 60.2 E 0 : 1.4e-08
Smith-Waterman score: 216; 29.839% identity (30.579% ungapped) in 124 aa overlap (1-121:85-208)

eco:b3 10 20 30
MGYQMLRGALKK-EAVS-APAPQVELAKSGRSFL

cdi:D1 LVWVTLTVFGATAVLTAYPSVLSAQLVGGTLLWNGTKLVRVARRQLGE
50 60 70 80 90 100 110

eco:b3 40 50 60 70 80 90 100
KGLLTNLANPKAIYFGSVFSLFVGDNVGTARWGIHALIIVETLAWFTV
psl:DI QGLATNLNSNPKVLYFAAIAPFLPTNPSLTLTALSIVVIVLSNL
120 130 140 150 160 170 180

eco:b3 110 120
IDGFAGALFAGFGIHLISR

cdi:D1 PDLVAGCFFIAGIGLIATRS
190 200 210

>>sme:SMc02484 putative amino acid efflux transmembrane protein (214 aa)
initn: 204 initl: 204 opt: 210 Z-score: 283.7 bits: 58.7 E 0 : 4e-08
Smith-Waterman score: 210; 31.967% identity (33.333% ungapped) in 122 aa overlap (1-118:88-208)

eco:b3 10 20 30
MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLK--

sme:SM MFHVTYTILGLGLIISQSIVLFNIVKWCVGAYLIYIGIKALRAGQTE
60 70 80 90 100 110 120

eco:b3 -CLLTNLANPKAIYFGSVFSLFVGDNVGTARWGIHALIIVETLAWFTV
psl:SM GLGFAANALNPKAVFFFSLFSTVVAHTPTVKFGYGFVMASLILINF
130 140 150 160 170 180 190

eco:b3 110 120
WIDGFAGALFAGFGIHLISR

sme:SM WIDRASQMVFIAGLKLATEKAA
200 210

>>opr:PBPR43511 hypothetical threonine efflux protein (218 aa)
initn: 211 initl: 211 opt: 210 Z-score: 283.6 bits: 58.8 E 0 : 4e-08
Smith-Waterman score: 210; 28.689% identity (30.172% ungapped) in 122 aa overlap (5-122:99-218)

eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNL
 ppr:PB LL1HQOPTLFALLQAAGGLYLLWLGI GAVRSVLMPIFRPTAHTETVTAP—QRI IANRKQALVKGFTTN1
 70 80 90 100 110 120 130
 eco:b3 40 50 60 70 80 90 100
 ANPKAI YFGSVFSLFVGDNVGTARWG FALIIVETLAWFTVVASLFA LPQMRRGYQRLAKWIDGFAGA
 ppr:PB LNPKALVFFFISLLSTI VPVDMSGKITAIAILWITSPLWFAMLA WLLTGKRLQQKIQQWTPYIDGICGV
 140 150 160 170 180 190 200
 eco:b3 110 120
 LFAGFG—IHLIIISR
 ppr:PB LFVTIGSMILLNLLVAR
 210

>>vch:VCD091 conserved hypothetical protein (222 aa)
Initn: 191 init1: 191 opt: 206 Z-score: 278.2 bits: 57.8 E0: 7.9e-08
Smith-Waterman score: 206; 27.826% identity (29.091% ungapped) in 115 aa overlap (1-111:87-200)

eco:b3 NGYQMLRGALIKEAVS—APAPQVELAKSGRSF
 vch:VC LVHL1SLSLG1SYLVKQQPHLFNLLQLAGGSYLLYLGAGALQSMAQKNASTPTHSPAPS1-LGNRQAF
 50 70 80 90 100 110 120
 eco:b3 LKGLTNLNLPKA1!YFGSVFSLFVGDNVGTARWG1FAL1!VETLAUFTVVASLFLPQURRGYQRLAK
 vch:VC TKGMTNLNLPKALVFFFSSLSSI1PASMSVSGKVAAA1LVGLSLTHFSCLAWLLTTSAHQRMQR1TR
 130 140 150 160 170 180 190
 eco:b3 WIDGFAGALFAGFGIHL1ISR
 vch:VC SVDS1CAAVF1LAGGV1LWQASRAIAQTFGW1
 200 210 220

>|at:Atu2633 rhtB; RhtB family transporter (204 aa)
initn: 200 initl: 200 opt: 201 Z-score: 272.0 bits: 56.5 E0: 1.8e-07
Smith-Waterman score: 201: 33.065% identity (35.345% ungapped) in 124 aa overlap (1-118:77-198)

eco:b3 MGYQMLRGALKKEAVSAPAPQVEL-AKSGRSFLK-
 atu:At MFHVTYTILGLGLIISQSIVLFNIVKWLGVAYLIYIGKALR-ACKTELPTAEGGEDGVRAKSQQTGLKA
 50 50 70 80 90 100 110
 eco:b3 —GLLTNLANPKAIYFGSVFSLFVGDNVGTARWGIFALIIVETLA-WFTVVASLFAFPQURRGYQRL
 atu:At FTLGFAANALNPKPVFFFLSIFSTVVHAHTPVGIKFG-YGLVMASCLIWVFVGVSLEMTPRMRAAFQRA
 120 130 140 150 160 170
 eco:b3 AKWIIDGFAGALFAGFGIHLIIISR
 atu:At SQWIDRTSGVVFIALGIKLATEKAA
 180 190 200

>>atc:AGR_C_4773 amino acid efflux-like protein (216 aa)
initm: 200 initl: 200 opt: 201 Z-score: 271.8 bits: 56.6 E0: 1.8e-07

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Smith-Waterman score: 201; 33.065% identity (35.345% ungapped) in 124 aa overlap (1-118:89-210)

eco:b3 10 20 30
MGYQMLRGALKKEAVSAPAPQVEL-AKSGRSFLK-
60 70 80 90 100 110 120

atc:AG NFHVTVTILGLGLIISQSIYLNFNIVKVKGVAYLIYIGIKALR-AGKTELPTAEGGEDGVRAKSQQTGLKA
60 70 80 90 100 110 120

eco:b3 40 50 60 70 80 90
---GLLTNLANPKAIYFGSVFSLFVGDNVGTARWGIHALIIVETLA-WFTVVASLFA[P]QMRGGYQLR
130 140 150 160 170 180 190

atc:AG FTLGFAANALNPKVFFLSIFSTVVVHATPVGKFG-YGLVMASCLILWFGVSLFMTTPRNRAAFQRA
130 140 150 160 170 180 190

eco:b3 100 110 120
AKWIDGFAGALFAGFGIHLIISR
200 210

>>ecc:c0448 yahN: resistance factor to homoserine/threonine, RhtB (224 aa)
initn: 204 initl: 204 opt: 201 Z-score: 271.6 bits: 56.6 E 0 : 1.9e-07

Smith-Waterman score: 201; 34.783% identity (37.209% ungapped) in 92 aa overlap (31-119:129-217)

eco:b3 10 20 30 40 50 60
MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIYFGSVFSLFVGDNVGTAR
100 110 120 130 140 150 160

ecc:c0 GAYLLWFAWCSSMRRNSTPQMSTLQQPIASPHVVFRRGLITDLSNPQTVLFFFISIFSVTLHAETPTWAR
100 110 120 130 140 150 160

eco:b3 70 80 90 100 110 120
WGIFALIIVETLAWFTVVASLFA[P]QMRGGY—QRLAKWIDGFAGALFAGFGIHLIISR
170 180 190 200 210 220

ecc:c0 LMAWAGIVLASIIWRVFLSQAFSLPAVRRRAYGRNQRVASRV—ICAIIGVFAFLRIYEVTQR
170 180 190 200 210 220

>>ecj:jw0320 yahN: resistance factor to homoserine/threonine, Rht (223 aa)
initn: 206 initl: 206 opt: 198 Z-score: 267.7 bits: 55.8 E 0 : 3.1e-07

Smith-Waterman score: 198; 32.584% identity (32.584% ungapped) in 89 aa overlap (31-119:128-216)

eco:b3 10 20 30 40 50 60
MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIYFGSVFSLFVGDNVGTAR
100 110 120 130 140 150 160

ecj:jw GGAYLLWFAWCSSMRRNSTPQMSTLQQPIASPHVVFRRGLITDLSNPQTVLFFFISIFSVTLNAETPTWAR
100 110 120 130 140 150 160

eco:b3 70 80 90 100 110 120
WGIFALIIVETLAWFTVVASLFA[P]QMRGGYQRLAKWIDGFAGALFAGFGIHLIISR
170 180 190 200 210 220

ecj:jw LMAWAGIVLASIIWRVFLSQAFSLPAVRRRAYGRNQRVASRVICAIIGVFAFLRIYEVTQR
170 180 190 200 210 220

>>eco:b0328 yahN: putative cytochrome subunit of dehydrogenase [K] (223 aa)
initn: 206 initl: 206 opt: 198 Z-score: 267.7 bits: 55.8 E 0 : 3.1e-07

Smith-Waterman score: 198; 32.584% identity (32.584% ungapped) in 89 aa overlap (31-119:128-216)

eco:b3 10 20 30 40 50 60
MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIYFGSVFSLFVGDNVGTAR
100 110 120 130 140 150 160

eco:b0 GGAYLLWFAWCSSMRRNSTPQMSTLQQPIASPHVVFRRGLITDLSNPQTVLFFFISIFSVTLNAETPTWAR
100 110 120 130 140 150 160

eco:b3 70 80 90 100 110 120
WGIFALIIVETLAWFTVVASLFA[P]QMRGGYQRLAKWIDGFAGALFAGFGIHLIISR
170 180 190 200 210 220

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eco:b0 LMAWAGIVLASI||WRVFLSQAFSLPAVRRAYGRMQRVASRV|GAI|GVFALRLIYEGVTQR
170 180 190 200 210 220

>>ece:Z0424 yahN: putative cytochrome subunit of dehydrogenase [K0:K0] (223 aa)
initn: 206 initl: 206 opt: 198 Z-score: 267.7 bits: 55.8 E0: 3.1e-07
Smith-Waterman score: 198: 32.584% identity (32.584% ungapped) in 89 aa overlap (31-119:128-216)

10 20 30 40 50 60
eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIYFGSVFSLFVGDNVGTAR
100 110 120 130 140 150 160

70 80 90 100 110 120
eco:b3 WGIFALIIIVETLAWFTTVVASLFAFPQMRGGYQRLAKWIDGFGALFAGFGIHLIISR

ece:Z0 LMAWAGIVLASI||WRVFLSQAFSLPAVRRAYGRMQRVASRV|GAI|GVFALRLIYEGVTQR
170 180 190 200 210 220

>>ecs:ECs0382 putative cytochrome subunit of dehydrogenase [K0:K0] (223 aa)
initn: 206 initl: 206 opt: 198 Z-score: 267.7 bits: 55.8 E0: 3.1e-07
Smith-Waterman score: 198: 32.584% identity (32.584% ungapped) in 89 aa overlap (31-119:128-216)

10 20 30 40 50 60
eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIYFGSVFSLFVGDNVGTAR
100 110 120 130 140 150 160

70 80 90 100 110 120
eco:b3 WGIFALIIIVETLAWFTTVVASLFAFPQMRGGYQRLAKWIDGFGALFAGFGIHLIISR

ecs:EC LMAWAGIVLASI||WRVFLSQAFSLPAVRRAYGRMQRVASRV|GAI|GVFALRLIYEGVTQR
170 180 190 200 210 220

>>cgl:NCgj0143 CglD146: putative threonine efflux protein (228 aa)
initn: 138 initl: 138 opt: 197 Z-score: 266.3 bits: 55.6 E0: 3.7e-07
Smith-Waterman score: 197: 35.398% identity (38.462% ungapped) in 113 aa overlap (9-119:108-213)

10 20 30 40
eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPK
80 90 100 110 120 130

50 60 70 80 90 100 110
eco:b3 AIIYFGSVFSLFVGDNVGTARWGIF—AIIIVETLAWFTTVVASLFAFPQMRGGYQRLAKWIDGFGALF
cgl:NC AVLFFGSVFAQFVRPDWIGIG—WSIFIGVFLTLTGLLWFVGFAVL--VRKLAAGLTRNGAIIDLITGVIF
140 150 160 170 180 190 200

120
eco:b3 AGFGIHLIISR

cgl:NC IGLGMPMIFEGVVVGIGGRVVG
210 220

>>stm:STM0365 yahN: putative transport protein [K0:K03329] (210 aa)
initn: 202 initl: 202 opt: 194 Z-score: 262.6 bits: 54.8 E0: 5.9e-07
Smith-Waterman score: 184: 31.461% identity (31.461% ungapped) in 89 aa overlap (31-119:115-203)

10 20 30 40 50 60
eco:b3 MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIYFGSVFSLFVGDNVGTAR
stm:ST GGAYLLWFANNSIRHOATPQSTLQTPIAAPWTIFFRRLMTDLSPQTVLFFISIFSVTSAETPTWAR

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80	90	100	110	120	130	140
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eco:b3 WGI~~FAL~~!!VETL~~AFTVV~~ASL~~FALP~~Q~~MRRG~~YQRLAKWIDGFAGALFAGFGIHLIISR
 70 80 90 100 110 120

stm:ST LMAWAGIVLSSVIWRIFLSQAFSLPAVRRAYGRIGRIASRVIGAIGMFALRLLYEGMTHR
 150 160 170 180 190 200 210

>>sty:STY0397 RhtC-like transporter (210 aa)
 initn: 202 init1: 202 opt: 194 Z-score: 262.6 bits: 54.8 E 0 : 5.9e-07
 Smith-Waterman score: 194; 31.461% identity (31.461% ungapped) in 89 aa overlap (31-119:115-203)

10	20	30	40	50	60
eco:b3	MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIYFGSVFSLFVGDNVGTAR				
sty:ST	GGAYLLWF AWNS SIRHQATPQ MSTL QTPAAPV T IF FR RGLMTDLSNPQT V LFFISIFS V TSAETPTWAR				
80	90	100	110	120	130 140

eco:b3 WGI~~FAL~~!!VETL~~AFTVV~~ASL~~FALP~~Q~~MRRG~~YQRLAKWIDGFAGALFAGFGIHLIISR
 70 80 90 100 110 120

sty:ST LMAWAGIVLSSVIWRIFLSQAFSLPAVRRAYGRIGRIASRVIGAIGMFALRLLYEGMTHR
 150 160 170 180 190 200 210

>>t2499 RhtC-like transporter (210 aa)
 initn: 202 init1: 202 opt: 194 Z-score: 262.6 bits: 54.8 E 0 : 5.9e-07
 Smith-Waterman score: 194; 31.461% identity (31.461% ungapped) in 89 aa overlap (31-119:115-203)

10	20	30	40	50	60
eco:b3	MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKAIYFGSVFSLFVGDNVGTAR				
stt:t2	GGAYLLWF AWNS SIRHQATPQ MSTL QTPAAPV T IF FR RGLMTDLSNPQT V LFFISIFS V TSAETPTWAR				
80	90	100	110	120	130 140

eco:b3 WGI~~FAL~~!!VETL~~AFTVV~~ASL~~FALP~~Q~~MRRG~~YQRLAKWIDGFAGALFAGFGIHLIISR
 70 80 90 100 110 120

stt:t2 LMAWAGIVLSSVIWRIFLSQAFSLPAVRRAYGRIGRIASRVIGAIGMFALRLLYEGMTHR
 150 160 170 180 190 200 210

>>mlo:m16377 threonine efflux protein (212 aa)
 initn: 198 init1: 172 opt: 194 Z-score: 262.6 bits: 54.8 E 0 : 5.9e-07
 Smith-Waterman score: 194; 30.400% identity (31.405% ungapped) in 125 aa overlap (1-122:88-211)

10	20	30
eco:b3	MGYQMLRGAL—KKEAVSAPAPQVELAKSGRSFL	
mlo:m1	IFWGFM ASTG ISALLARYAQ ALL VLQVF G GLYLLFLA FRAG R SA LT N EKLAVRASTDQ VAL SR-GELYR	
60	70	80 90 100 110 120

40	50	60 70 80 90 100
eco:b3	KGLLTNLANPKAIYFGSVFSLFVGDNVGTARWGI F !!VETL AFTVV ASL FALP Q MRRG YQRLAKW	
mlo:m1	KGLMMH LN ANPKSVL W IA L VTLG G P N SS W Q S AA L G G C A ILSVT I FCGYA I V F STPPM V ALY Y RR C RRW	
130	140	150 160 170 180 190

110	120	
eco:b3	1DG FAG ALFAGFGIHLIISR	
mlo:m1	I E SSL L AM FF A G LR M LL S R M	
200	210	

>>pae:PA4757 conserved hypothetical protein [KO:K03329] (216 aa)
 initn: 152 init1: 112 opt: 192 Z-score: 259.9 bits: 54.4 E 0 : 8.4e-07
 Smith-Waterman score: 192; 36.000% identity (39.130% ungapped) in 125 aa overlap (1-118:89-210)

	10	20	30			
eco:b3	MGYQILRGALKK	EAVSAPAPQVELAKSGRSF				
pae:PA	AVLMLLSALGVASLLKAEPMLF	IGLKYLGAAYLFYLGVGILRGAWRKLRNPEATAAQAEQVVDVHQP	F			
60 70 80 90 100 110 120	100 110 120	100 110 120				
eco:b3	LKGLLTNILANPKAI	IYFGSVFSLFVGDNVGTATARWGI	FALI	I	IVETLAHFTVVASLFA	LPQWRRGYQR
130 140 150 160 170 180 190	130 140 150 160 170 180 190	130 140 150 160 170 180 190				
pae:PA	RKALLLSSLNPKAIIFFISFFI	QFVDPGYYAPPGLSFLVLAVI	LELVSALYSFL	I	FTGVRLAAWFRRQR	
eco:b3	LAKWIDGFAGALFAGFGIHLISR					
200 210	200 210	200 210				
pae:PA	LAAGATSGVGVGALFVGFGVKLATATLS					

>>pa:PA2929 hypothetical protein (204 aa)
initn: 190 initl: 190 opt: 191 Z-score: 258.8 bits: 54.1 E0: 9.6e-07
Smith-Waterman score: 191; 31.356% identity (31.897% ungapped) in 118 aa overlap (1-118:84-199)

<p>eco:b3</p> <p>pae:PA TVHVGYSILGVGVLVRESLALFTALKLACAAAYLVFLGLPULLA—REDSVAAAAGGAGVSSWAMLRSGF</p> <p>50 60 70 80 90 100 110</p> <p>eco:b3 LTNALNPKAIIYFGSVFSLFVGDNVGTARWGIHALIIVETLAHFTVVASLFALPQMRGGYQLRLAKWIDG</p> <p>110 120 130 140 150 160 170 180</p> <p>pae:PA LTNALNPKTCLFVVSLFMQVIDPHTALPAQLGYCAFIALAHVAWFLVACFLSSPAVRGRLLRFRRRIDQ</p> <p>120 130 140 150 160 170 180</p> <p>eco:b3 FAGCALFAGFGIHLLISR</p> <p>110 120</p> <p>pae:PA FFGALLVGFVLLGAKSP</p> <p>190 200</p>	<p>10 20 30</p> <p>MGYQNLRGALKKEAVSAPAPQVELAKSGRSFLKGL</p>
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>>>PBPRA1361 hypothetical homoserine/homoserine lactone efflux (209 aa)
initn: 178 initl: 178 opt: 191 Z-score: 268.7 bits: 54.1 E(0): 9.7e-07
Smith-Waterman score: 191; 37.113% identity (40.449% ungapped) in 97 aa overlap (30-122;116-208)

	10	20	30	40	50	60		
eco:b3	MGYQMLRGALKKEAVSAPAPQVELAKSGRSFLKGTLTNLANPKAIYFGSVFSLFVGDN~VGT							
ppr:PB	VYLFWLGVSNIKNGLNISLLKFDSSQNTKKTSINSFFKGLLTNLLNPKIVLFYLSIFPQFISPQHULAQ	90	100	110	120	130	140	150
eco:b3	TARWGIHALIIVETLAWFTVVASLFA—LPQMRRGYQRLAKWIDGFAGALFAGFGIXLIISR	70	80	90	100	110	120	
ppr:PB	SMALGITHALVVAS—WFLWVI-LFSVRLKSMLTS-SKVAKWLNIVSGGLFISFGVTLASTRL	160	170	180	190	200		

>>cef:CEO145 conserved hypothetical protein (234 aa)
initn: 149 initl: 149 opt: 191 Z-score: 258.2 bits: 54.2 E 0 : 1e-06
Smith-Waterman score: 191: 35.922% identity (38. 947% ungapped) in 103 aa overlap (19-179:125-221)

eco:b3 MGYQMLRGALIKKEAVSAPAPQVELAKSGRSFLKGLLTNLANPKA || YFGSVFS.
 cef:CE VRSWWGQRITARQAGDAVERVLEGQDGPGFGSPGVLGAR—RALRTGIAATNLSNPKAVLFFGSVFA

90	100	110	120	130	140	150
60	70	80	90	100	110	120
eco:b3 LFVGDNVGTTARWCIF--ALIIVETLAWFTVVASLFAFPQMRRGYQRLAKWIDGFAGALFAGFGIHLIIS						
cef:CE QF1TPDMVGVG--WSIPLAVFLILYGLVWFLGFAVLVRSAAR--ITRNAAVIDLFTGVIFIALGQFMVWQ						
160	170	180	190	200	210	220

eco:b3 R

cef:CE GVVIGIGSWILG
 230

>>eca:ECA3867 putative LysE-type translocator (204 aa)
 initn: 180 initl: 180 opt: 190 Z-score: 257.5 bits: 53.8 E 0 : 1.1e-06
 Smith-Waterman score: 190; 30.545% identity (33.043% ungapped) In 124 aa overlap (1-120:85-203)

10	20	30
MGYQML—RGALKKEAVSAPAPQVELAKSGRSFLK		
eco:b3		

50	60	70	80	90	100	110
eca:EC ATHMAYCVAGLAVVTTTPWLNFNLKYAGAAYLIWIGIGQALFTRGGSIQDVSNLTQQSVSLKKA—FLQ						
50	60	70	80	90	100	110

40	50	60	70	80	90	100
eco:b3 GLLTNLNPKAIIYFGSVFSLFVGDNVGTAR-WGIFALII-VETLAWFTVVASLFAFPQMRRGYQRLAK						
eca:EC GYLGNLLNPKATLFFLAMFTQVLNITHSGIGEKWL—YAMIIWLLSLVWPLLVLFQSEPVRRGLAKVQK						
120	130	140	150	160	170	180

110	120
eco:b3 WIDGFAGALFAGFGIHLIISR	
eca:EC LVOKLLGTYLIALGIKVALG	
190	200

>>pae:PA4507 hypothetical protein (210 aa)
 initn: 197 initl: 116 opt: 182 Z-score: 246.8 bits: 51.9 E 0 : 4.5e-06
 Smith-Waterman score: 182; 35.294% identity (42.857% ungapped) In 136 aa overlap (1-122:83-208)

10	20	30
MGYQMLRG—ALK-KEAVSAPA-PQVELAKSGRS		
eco:b3		

50	60	70	80	90	100	110
pae:PA ACHVLMATGLALLFRTAPWTFDLVRLLGAVYLAWLGLQMLRGGLALPTSDAGSAPVPHADR—RA						
50	60	70	80	90	100	110

40	50	60	70	80	90	
eco:b3 FLKGLLTNLNPKAIIYFGSVFSLFVGDNVGTAA-RWGIFALII-VETLAWFTVVASLFAFPQMRRGY—						
pae:PA LLRGLLTNLLNPKALLFCVSLLPQFVSPEAGSLAVQFAALGTVLVLVGLAFDCA—YALAGGRILGRWLA						
120	130	140	150	160	170	180

100	110	120
eco:b3 ——QRLAKWIDGFAGALFAGFGIHLIISR		
pae:PA SRPRAQRQLQQW—GFGG-LIIGFGVRLALLRQL		
190	200	210

>>cvi:CV3240 rhtC; Threonine efflux protein (207 aa)
 initn: 171 initl: 171 opt: 181 Z-score: 245.6 bits: 51.6 E 0 : 5.2e-06
 Smith-Waterman score: 181; 25.620% identity (25.833% ungapped) In 121 aa overlap (1-120:86-206)

10	20	30
MGYQMLRGALKK-EAVSAPAPQVELAKSGRSFLKG		
eco:b3		

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cvl:CV GLYALAAAQGLAMVMAHPLLKIISSLGAAYLVWLGVQQLRAASRPARAASGETAAAPTSWRAARTG
60 70 80 90 100 110 120

eco:b3 40 50 60 70 80 90 100
LLTNLANPKAIYFGSVFSLFVGDNVGTARWGIHALIIVETLAWFTVVASLFLPQMRGGYQRLAKWID
130 140 150 160 170 180 190

110 120
eco:b3 GFAGALFAGFGIHLLISR
200
cvl:CV GCGGALMLLLGLRILVV

>>son:S00765 threonine efflux protein, putative (234 aa)
initn: 184 initl: 184 opt: 180 Z-score: 243.7 bits: 51.5 E 0 : 6.7e-05
Smith-Waterman score: 180; 26.316% identity (27.027% ungapped) in 114 aa overlap (9-119:115-228)

eco:b3 10 20 30 40
MGYQMLRGALKKEAVSAPAPQVELAKS—GRSFLKGLLTNLA

son:S0 ASYLAVMGMFGALKATIAFFRKPKRLLKGEEAESSVATEAQANTGDNSQTKAEKSLSPRGFMGLYTNL
80 90 100 110 120 130 140

eco:b3 50 60 70 80 90 100 110
NPKAIIYFGSVFSLFVGDNVGTARWGIHALIIVETLAWFTVVASLFLPQMRGGYQRLAKWIDGFAGAL

son:S0 NPKAIVFFTLFSALITPSVTPATKVAAALVLVLSIWFEGFLALMLSKAKVQQKMKQRITPIIDAVIGVI
150 160 170 180 190 200 210

120
eco:b3 FAGFGIHLLISR
220 230
son:S0 FMSVALAIVSNLLV

>>cef:CE2245 putative threonine efflux protein (224 aa)
initn: 222 initl: 177 opt: 179 Z-score: 242.8 bits: 51.2 E 0 : 7.7e-06
Smith-Waterman score: 198; 28.462% identity (31.092% ungapped) in 130 aa overlap (1-119:85-214)

eco:b3 10 20
MGYQMLRGALKK—EAVSAPAPQ—VEL

cef:CE TVWVTLTVVGAATLLTTYPDILGVIQLVGGGYLTWGYRMGRGAVRELLDARAFRFNSATRPIPDAVAAL
50 60 70 80 90 100 110

eco:b3 30 40 50 60 70 80 90
AKSGRSFLKGLLTNLANPKAIYFGSVFSLFVGDNVGTARWGIHALIIVETLAWFTVVASLFLPQMR

cef:CE GTPGQAYRQQMATNLSNPKVINYFAALAPLMPANPSLAVALTIIAIIVQTNVVFTFCIVSTERIRK
120 130 140 150 160 170 180

100 110 120
eco:b3 GYRLAKWIDGFAGALFAGFGIHLLISR

cef:CE AVLRAFPVFDGVAAVFIAVGLTLIYEGASQLLG
190 200 210 220

>>plu:plu1236 unnamed protein product; similar to amino acid effl (211 aa)
initn: 177 initl: 177 opt: 178 Z-score: 241.5 bits: 50.9 E 0 : 8e-06
Smith-Waterman score: 178; 26.230% identity (27.350% ungapped) in 122 aa overlap (1-119:88-207)

eco:b3 10 20 30
NGYQMLRGALKKEAVSAPAPQVELAKSG-RSFLKG

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